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<!--StartFragment-->RESULT 3
AB181388
LOCUS       AB181388             11991 bp    DNA        linear    BCT 05-OCT-2006
DEFINITION   Brevundimonas sp. SD212 carotenoid biosynthesis gene cluster (orf1,
              crtW, crtY, crtI, crtB, orf6, orf7, crtE, idi, crtZ, crtG, orf12),
              complete cds.
ACCESSION    AB181388
VERSION      AB181388.1  GI:67003493
KEYWORDS     .
SOURCE       Brevundimonas sp. SD212
ORGANISM     Brevundimonas sp. SD212
              Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
              Caulobacteraceae; Brevundimonas.
REFERENCE    1
AUTHORS      Nishida,Y., Adachi,K., Kasai,H., Shizuri,Y., Shindo,K., Sawabe,A.,
              Komemushi,S., Miki,W. and Misawa,N.
TITLE        Elucidation of a carotenoid biosynthesis gene cluster encoding a
              novel enzyme, 2,2'-beta-hydroxylase, from Brevundimonas sp. strain
              SD212 and combinatorial biosynthesis of new or rare xanthophylls
JOURNAL      Appl. Environ. Microbiol. 71 (8), 4286-4296 (2005)
PUBMED       16085816
REFERENCE    2 (bases 1 to 11991)
AUTHORS      Nishida,Y. and Misawa,N.
TITLE        Direct Submission
JOURNAL      Submitted (08-JUN-2004) Norihiko Misawa, Marine Biotechnology
              Institute, Applied Science of Molecular Design; 3-75-1, Heita,
              Kamaishi-shi, Iwate 026-0001, Japan
              (E-mail:norihiko.misawa@mbio.jp, Tel:81-193-26-6581,
              Fax:81-193-26-6584)
FEATURES
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Query Match      100.0%;   Score 774;   DB 14;   Length 11991;
Best Local Similarity 100.0%;   Pred. No. 2.2e-170;
Matches 774;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy      61  CTGCTGGTCGGCGCGCGGCCCATGGGCTGCTGTGGGCGGGGCGGGCGGGGACGGGCG 120
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Qy      121 CTGAACCTGCGGCGCGCGCGCATGAAGCGCATCCGCGCGAGATCGTCGCCCTCCCTGATC 180
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Db      10868 CTGAACCTGCGGCGCGCGCGCATGAAGCGCATCCGCGCGAGATCGTCGCCCTCCCTGATC 10927
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Qy      181 GCCTGCCCCATCTACGCCCTGCCGGCGGCCCTGGTGCTGGAGCTGTGGAAGCGGGGCGGG 240
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Db      10928 GCCTGCCCCATCTACGCCCTGCCGGCGGCCCTGGTGCTGGAGCTGTGGAAGCGGGGCGGG 10987
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Qy      361 CGCGTCTTCGGCTGGGCCCATGCCGAACACACCGGTGCGCGACCCACGCGCTTCGCC 420
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<!--EndFragment-->